

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
Subject: gi|4557225 ref|NP_000005.1| alpha-2-macroglobulin precursor sp|P01023|A2MG_HUMAN ALPHA-2-MACROGLOBULIN
PRECURSOR (ALPHA-2-M) pir||MAHU alpha-2-macroglobulin precursor - human >gb|AAA51551.1| (M11313) alpha-2-macroglobulin
precursor [Homo sapiens] (SEQ ID NO: 23)
Length = 1474

Score = 2714 (960.4 bits), Expect = 1.7e-281, P = 1.7e-281
Identities = 596/1494 (39%), Positives = 874/1494 (58%)

Query:	13	LLGLMALSPAIAEELPNYLVTLPARLNFPSPQKVCLDSPGYSDVKFTVTLETKDKTQK	192
		LLL +L +++ + P Y+V +P+ L+ + +K C+ LS V + +LE+ +	
Sbjct:	14	LLVLLPTDASVSGK-PQYMLVLPVPSLLHTTETTEKGCVLVLYNETVTVSASLESVRGNRS	72
Query:	193	LLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEEKKKVLIQRQNGTFV	372
		L + LHC++F VP + EEV + V G F+++ V+++ + + FV	
Sbjct:	73	LFTLEAENDVLHCVAFAVPK-SSSNEEVFLTVQVKGPTEFKKRTTVMVKNEDSLFFV	131
Query:	373	QTDKPLYTPGQOVVFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLS	552
		QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S	
Sbjct:	132	QTDKSIYKPGQTVKFRVWSMDENFHLNELIPLVYIQDPKGNRIAQWQSFQLEGGLKQFS	191
Query:	553	FQLAPEAMLGTVTVAAVE---GKTFGTFSVEEVVLPKFKVEVVEPKELSTVQESFLVKIC	723
		F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C	
Sbjct:	192	FPLSSEPFQGSYKVVVQKSGGRTEHPFTVEEFVLPKFVQVTVPKIITILEEEMNVSV	251
Query:	724	CRYTYGKPMLGAVQVSVCKANTYWYREVEREQLPDKCRNLSGQTDKTCGFSAPVDMATF	903
		YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F	
Sbjct:	252	GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCERFSGQLNSHGCFYQQVKTKVF	309
Query:	904	DLIGYAYSHQINIVATVVEEGTGVVEANATQNIYISPMGSMTFEDTSNFIHPNFPFSGKI	1083
		L Y +++ A + EEGT VE Q+ I+ + ++F + + PF G++	
Sbjct:	310	QLKRKEYEMKLHTEAQIQEEGTVVVELTGRQSSBITRTITKLSFVKVDSHFPRQGI	369
Query:	1084	RVRGHDDSLKKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLETSGWNGTVDVLEKGFQM	1263
		R+ + N ++F I G + TD +GL F++ T+ GT +++ ++	
Sbjct:	370	RLVDGKGVPINPKVIF--IRGNEANYYSNATTDHGLVQFSINTTNVMGTSLTVRVNYKD	427
Query:	1264	EDLVNPEQVPVRYQNAYLHLRPFYSTRSFLGTHRLNGPLKCGQPQEVLDVYIDPADA	1443
		Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++	
Sbjct:	428	RSPCYGYQWVSEEHBAHHTAYLVFSPKSFVHLEPMSHELPCGHTQTQVAHYILNGGTL	487

Fig 1A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

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Query: 1444 SPDQEISFSYVLIGKGLVMEQKHLNSKKKGLKASFSLSLTFTSRLAPDPSLVIYAIFF 1623
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKKLSFYLLIMAKGIVRTGTHGLLVKQEDMKGHFSIPVKSIDIAPVARLLIYAVLP 547

Query: 1624 SGGVADKIQFSVGMCFDNQVSLGFSQSPQLPGAELQLQAAPGSLCALRAVDSEVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDLSFSPSQSPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFPFVYGHYPYQVAEYDQCPVSGPWFPPQLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSTNEKDMYSFLEDMGLKAPTNSKIRKPKMCPQLQYEMHGPGLRVGFYESDVMMGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITWKA MSFC 2304
      GH P H VR+YFPETW+WDL + ++G V VTVPD ITEWKA +FC
Sbjct: 716 GHARLVHVEEP-HT---ETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDITTEWKAGAF 771

Query: 2305 TSQSRGFLSPTVGLTAFKPPFFVDLTLPYSVVRGESFRLTATIFNYLKDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLGISSTASLRAFPFPFFVELTMPYSVIRGEAFTLKATVLNLYLPKIRVSVQLEAS 831

Query: 2485 HEYQLESWADTSQSSCLCADDKTHHWNITAVKLGHNFTTISTKILDSNEPCGGQKGFVP 2664
      + Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFVSAEALAESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGKVASESLSLELPVDIVPDSTKAYVTVL 2844
      + GR DT+IKP+LV+PEG+ E T +SLLCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVEPEGLEKETTFNLSLLCPSGGEVSEELSLKLPNPNVEESARASVSVL 951

Query: 2845 GKQLEILDSEKRRMEAAKVMRDIMGTAQNLDGLVQMPSGGEGQNMVLFAPIIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYGCGEQNMVLFAPNIYVLDYL 990

Query: 3025 EKAGLTPEIRSRVAVGLEIGYQKELMYKHSNGSYSAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT E++S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEVKS KAIGYLNLTGYQRQLNYKHYDGSYSTFGERYGRNQGNLTWLTAFVLKTFA 1050

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Fig. 1B

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

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Query: 3199 QAQKFIIDPKNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDDEVSLTAYVTAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAYIFIDEAHITQALIWLSQRQKDNCGFRSGSLNNAIKGVEDEVTL SAYITIAL 1110

Query: 3379 EMGKDVDPMVSQGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EIPLTVTHPVVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTPSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKKDINSVHWERPQKPKAPVGHFYEPAQPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIVAWLAKQHNAYGGSSTQDTVVVALQALAKY-ATTAYMPSEENLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGSSTQDTVVVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWTQQNAQGGSSTQDTVVVALHALSKYGAATFTRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQODTLPNVPGMYTLEASGQGCVVQTVLRYNLPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLLOQVSLPELPGEYSMKVTGEGCVLQTSKYNILPEKEEFPFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNMAIVEVKMLSGFSPMEGTNQLLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRASNMAIVDKMVSGFIPKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDTLNIYLDLIKNTQTYTFTISQSVLVTNLKPAATIKVYDYLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVYDY F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYDETDEFAIAEY 1463

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FIG. 1C

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. (SEQ ID NO 24)
Length = 1474

Score = 2699 (955.2 bits), Expect = 3.2e-280, P = 3.2e-280
Identities = 596/1494 (39%), Positives = 870/1494 (58%)

Query: 13 LLLGMLALSPAIAEELPNYLVTLPARLNFPSPQVKCLDLSPGYSDVKFTVTLETYKDKTQK 192
Sbjct: LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Query: 13 LLLLVLPPTDASVSGKPQYMLVLPVPSLLHTETTEKGCVLLSYLNETVTVSASLESVRGNRS 72
Sbjct: L L L L L V L P T D A S V S G K P Q Y M L V L P V P S L L H T E T T E K G C V L L S Y L N E T V T V S A S L E S V R G N R S
Query: 193 LLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVNNNISFEKKKKVLIQRQNGTFV 372
Sbjct: L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Query: 73 LFTDLEAENDVLHCVAFAVPK-SSSNEEVMFLTVQVKGPTQEFKKRTVMVKNEDSLFFV 131
Sbjct: L F T D L E A E N D V L H C V A F A V P K - S S S N E E V M F L T V Q V K G P T Q E F K K R T V M V K N E D S L F F V
Query: 373 QTDKPLYTPGQQVYFRIVTMDSNFVNDKYSMVLELQDPNSNRIRIAQWLEVVPEQGIVDLS 552
Sbjct: QTDK +Y PGQ V FR+V+MD NF P+N+ +V +ODP NRIAQW E G+ S
Query: 132 QTDKSIYKPGQTVKFRVSMDENFHLNELIPLVIQDPKGNRIQWQSFQLEGGLKQFS 191
Sbjct: Q T D K S I Y K P G Q T V K F R V S M D E N F H L N E L I P L V I Q D P K G N R I Q W Q S F Q L E G G L K Q F S
Query: 553 FQLAPEAMLGTYTVAAE---GKTGFTSVEEYVLPKPKVEVVEPKELSTVQESFLVKIC 723
Sbjct: F L + E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Query: 192 FPLSSEPFQGSYKVVVQKKSQGRTEHPFTVEEFVLPKFEVQVTVPKIITILEEEMNV SVC 251
Sbjct: F P L S S E P F Q G S Y K V V V Q K K S Q G R T E H P F T V E E F V L P K F E V Q V T V P K I I T I L E E E M N V S V C
Query: 724 CRYTYGKPMLGAVQSVQCANTYWYREVEREQLPDKCRNLSGQTDKTCGCFSAFVDMATF 903
Sbjct: YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Query: 252 GLYTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCEKFSQGLNSHGCFYQQVKTKVF 309
Sbjct: G L Y T Y G K P V P G H V T V S I C R K Y S D A - - S D C H G E D S Q A F C E K F S Q G L N S H G C F Y Q Q V K T K V F
Query: 904 DLIGAYSHQINIVATVVEEGTGVEANATQNIYISPMGSMTEFDTSNFYHPNFPFSGKI 1083
Sbjct: L Y +++ A + EEGT VE Q+ I+ + ++F + + PF G++
Query: 310 QLKRKEYEMKLHTEAQIQEEGTVELTGRQSSSEITRTITKLSFVKVDSHFRQGIPIFFGQV 369
Sbjct: Q L K R K E Y E M K L H T E A Q I Q E E G T V E L T G R Q S S S E I T R T I T K L S F V K V D S H F R Q G I P I F F G Q V
Query: 1084 RVRGHDDSF LKNHLVFLVIYGTNGTFTNQTLVTDNGLAPFTLETSGMNGTVDVSLGKFQM 1263
Sbjct: R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Query: 370 RLVDGKGVPIPNKVIF--IRGNEANYYSNATDEHGLVQFSINTTNVMGTSLTVRVNYKD 427
Sbjct: R L V D G K G V P I P N K V I F - - I R G N E A N Y Y S N A T D E H G L V Q F S I N T T N V M G T S L T V R V N Y K D
Query: 1264 EDLVNPEQVPYRYQNAYLHLRPFYSTTRSLGIHRLNGLPKCGQPQEVLDVYVIDPADA 1443
Sbjct: Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Query: 428 RSPCYGYQWVSEEEHAAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTQVQAHVILNGGTL 487
Sbjct: R S P C Y G Y Q W V S E E E H A A H T A Y L V F S P S K S F V H L E P M S H E L P C G H T Q T Q V Q A H V I L N G G T L
Query: 1444 SPDQELSFYYLICKGLVMEGQKHLNKKKGLKASFSLSLTFTTSRLAPDPSLVIYAIFP 1623
Sbjct: +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Query: 488 LGLKKLSFYLLIMAKGGIVRTGTHGLLVQEDMKGHFISISIPVKSDIAPVARLLIYAVLP 547
Sbjct: L G L K K L S F Y L L I M A K G G I V R T G T H G L L V Q E D M K G H F I S I S I P V K S D I A P V A R L L I Y A V L P

Fig. 2A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

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Query: 1624 SGGVVADKIQFSVGMCFDNOVSLGFSFSPQQLPGAEEVLQQAAPGSLCALRAVDSEVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDLSFSPQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFFFWYGHYPYQVAEYDQCPVSGPWDFPQPLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPAEELSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSTNEKDMYSFLEDMGLKAFNSKIRKPKMCPQLQQYEMHGPGLRVGFYESDVMGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEMKAMSFC 2304
      GH P H VR+YF ETW+WDL + ++G V VTPVD ITEWKA +FC
Sbjct: 716 GHARLVHVEEP-HT--ETVRKYFAETWIWDLVWNSAGVAEVGVTPDPTITENKAGAFC 771

Query: 2305 TSQSRGFLSPTVGLTAFKPFVVDLTLPSVWVRGESFRLTATIFNYLKDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PEFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLGISSASTASLRAFQPFVVELTMPYSVIRGEAFTLKATLVNLYLPKIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKATHWNITAVKLGHINFTISTKILDSNEPCGGQGFVP 2664
      + Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPVEKEQAPHCICANGRQTVSAVTPKSLGNVNFVTSAALESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGVASESVSLELPVDIVPDSKAYVTVL 2844
      + GR DT+IKP+LV+PEG+ E T +SLCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVSELSKLPNPNVVEESARASVSVL 951

Query: 2845 GKQLEILDSEKRRMEAAKVVWRDIMGTALQNLQGLVQMPSGCGEQNMVLFAPIIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYGCGEQNMVLFAPNIYVLDYL 990

Query: 3025 EKAGILLTEEIRSAVGFLGIGYQKELMYKHSNGSYSAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT EI+S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEIKSKAIGYLNLTGYQRLNYKHVDGSYSTFGERYGRNQNTWLTAFVLKTF 1050

Query: 3199 QAQKFIFIDPKNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDDEVSLTAVVTAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAVIFIDEAHITQALIWLSQRQKDNCGCFRSSGSLNNAIKGGVEDEVTL SAYITIAL 1110

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Fig. 2B

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: 3379 EMGKDVPMSVQGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EILLTVHPVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKREVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTPSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L++++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKDNSVHWERPQPKAPVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIVAWLAKQHNA YGGFSSSTQDTVVVALQALAKY-AFTAYMPSEEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSSTQ TVVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWIWKQNAQGGFSSSTQHTVVVALHALSKYGAATFTRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQDDTLPNVPGMYTLEASGGCGVYVQTVLRYNILPPTNMKTFSLSV EIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCVY+QT L+YNI LP F+L V+
Sbjct: 1290 FQVDNNRLLQQVSLPELPGEYSMKVTGCGCVYLTQSLKYNILPEKEEFPFALGVQTL P 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSVYGSRSSNNMAIVEVKMLSGFSPMEGTNQLLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRSSASNMAIVDKMVSGFIP LKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDTLNIYLDLIKNTQTYTFTISQSVLVNLPKPA TIKVYDY YLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVVDY Y F +++Y
Sbjct: 1410 VSSNHVLIYLDKRVSNQTL SLFFTVLQDVPVRDLKPAIVKVYDY YETDEFAIAEY 1463

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FIG. 2C

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
OVOS_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
Subject: >sp|p20740|OVOS_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >pir||A20872 ovostatin precursor - chicken
>emb|CAA55384.1| (X78801) ovomacroglobulin, ovostatin [Gallus gallus] (SEQ ID NO: 41)
Length = 1473

Score = 1300 (462.7 bits), Expect = 6.1e-135, Sum P(2) = 6.1e-135
Identities = 297/849 (34%), Positives = 457/849 (53%), Frame = +3

Query: 96 VYKFVPVSPTRKMAQALLGLMLALSPAIAEEL-PNYLVTLPARLNFPSVQKVCLDLSPGYS 272
+ F ++ KMW + +L +L L A +E P Y++ +PA L S +VCL
Sbjct: 9 ILSFFCLTVRKMWLKFILAILLLHAAAGKEPEPQYVLMVPAVLQSDSPSQVCLQFFNLNQ 68

Query: 273 DVKFTVTLETQDKTKLLEYSGLKRRHLHCISFLVPPPPAGGTEEVATIRVSGVGNISFE 452
+ V LE + E + L C++F++PP + +A I + G +
Sbjct: 69 TISVRVVLEYDTINTTIFEKNTTNSGLQCLNFMIPPVT--SVSLAFISFTAKGTTFDLK 126

Query: 453 EKKKVLIIQRQNGTFVQTDKPLYTPGQQVYFRIVTMDSNFVPNDKYSMVLELQDPNSNRI 632
E++ V+I + FVQTDKP+Y PGQ V FR+V +D NF PV + Y ++ +QDP +NRI
Sbjct: 127 ERRSVMIWNMESFVVFVQTDKPIYKPGQSVMFVRVALDFNFKPQVQEMYPLIAVDQPNRI 186

Query: 633 AQMLEVVPEQGIVDLSFQLAPEAMLGTYTVAAE--G-KTFGTFSVEEYVLPKFKVEVVE 803
QW V E IV + F L E +LG Y + V + G +T +F VEEVLPKF V V
Sbjct: 187 FQWQNTSEINIVQIEPPLTEEPILGNKYIIVTKKSGERTSHSFLVEEYVLPKFDVTVTA 246

Query: 804 PKELSTVQESFLVKICCRYTYGKPMGLGAVQVSVCKANTYVYREVEREQLPDKCRNLSCQ 983
P L+ + VKIC YTYG+P+ G VQ+SVK+ ++Y R + C++ +
Sbjct: 247 PGSLTVMDSSELTWKICAVITYGQPVVEGKVQLSVCRDFDSYG----RCKSPVCQSFTKD 301

Query: 984 TDKTGCFSAPVDMATFDLIGYAYSHQINIVATVVEEGTGV EANATQNIYISPMGSMTFE 1163
D GC S + F+L Y +++ A V E+ ATQ+I I+ M S+ FE
Sbjct: 302 LDTDGCLSHILSSKVFELNRIGRYKRNLDVKAIVTEKEQVCNLTATQISITQVMSSLOFE 361

Query: 1164 DTSNPHYHPNFPFSGKIRVRGHDDSF LKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLET 1343
+ + Y P+ G+I++ D+S + N ++ L + N T N T TD NG+APF+++T
Sbjct: 362 NVDDHYRRGIPYFGQIKLVLDKDNISPISNKVIQLFVNKN-THNFT--TDINGIAPFSIDT 418

Fig 3A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
OVOS_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

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Query: 1344 SGWNGTDVSLGKFKQMEDLVYNPEQVPRYYQNAVYHLRPPFYSTTRSLGIHRLNGLKCG 1523
      S ++SL+ ++ D ++ + Y +A L ++ YS T SF+ I L + CG
Sbjct: 419 SKIFDPELSLKALYKTSQCHSEGWIEPSYDASLSVQRLYSWTSSVRIEPLWKDMSCG 478

Query: 1524 PQEVLVDYYIDPADASPDQEIFSYLIGKSLVMEQKHLNSKKKGLKASFSLSLTFT 1703
      Q + + V Y ++ ++F Y + KG +V+ G+ +N + +F + L
Sbjct: 479 QKRMITVYYILNTEGYEHINIVFYVGMAGKIVLTGEIKVNIQADQ-NGTFMIFLVVN 537

Query: 1704 SRLAPDPSLVIYAIFFPSGGVVADKIQFSVEMCFDNQVSLGFSQQLPGAELQLQAAP 1883
      ++AP L++Y + P+ +VAD ++FS+E CF N+V L FS Q L + V L ++AA
Sbjct: 538 EKMAPALRLLVYMLHPAKELVADSVRFSEKCFKKNVQLQFSEKQMLTTSNVSLVIEAAA 597

Query: 1884 GSLCALRAVDESLLLLRPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWDFPQPL 2063
      S CA+RAVD+S+LLL+ + ELS ++Y + P Q ++ + D PQ
Sbjct: 598 NSFCAVRAVDKSMMLLKSETLSAETIYNLHPI-----QDLQGYIFNGLNLE---DDPQ-- 648

Query: 2064 IDPMFQGHSS-QRSIIWRPFSFSE-GTDLFSFPRDVGLKILSNAKIKKPVDCSH---RSPE 2228
      DP + + +RP S G D++ F RD+G+K +N+KI++P C+ R P
Sbjct: 649 -DPCVSSDDIFHKGLYRPLTSGGLGPDVYQFLRDMGMKFFFTNSKIROPTVCTREIVRPPS 707

Query: 2229 YSTAMG--AGGHPF-----AFESSTPLHQAEDSQVRQRYFPETWLWDLFPIGNSGEAVH 2387
      Y G A H + A E H E +R++FPETW+WD+ I ++GK +V
Sbjct: 708 YFLNAGFTASTHVVKLSAEVAREERGRHILET--IREFFPETWIWDILINSTGKASVS 765

Query: 2388 VTVPDAITEWKAMSFCTSQSRGFGLSPTVGLTAFKPPFFVDLTLPYSVVRGESFRLTATIF 2567
      T+PD ITEWKA +FC + GFG+S LTAF+PFFVDLTLPYS++ GE F + A +F
Sbjct: 766 YTIPDTITWKASAFCEELAGFGMSVPATLTAFQPPFFVDLTLPYSIHGEDFLVRANVF 825

Query: 2568 NYLKD CIRV 2594
      NYL CI++
Sbjct: 826 NYLNHC IKI 834

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Fig 3B

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. SEQ ID NO: 24
Length = 1474

Score = 1289 (458.8 bits), Expect = 5.6e-134, Sum P(2) = 5.6e-134
Identities = 300/834 (35%), Positives = 448/834 (53%), Frame = +3

Query: 141 LLLGMLALSPAIAEELPNYLVTLPARLNFPSPQKVCLDSPGYSDVKFTVTLETKDKTQK 320
 LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Sbjct: 13 LLLLVLPPTDASVSGKPQYMLVPSLLHTETTEKGCVLISYLNETVTVSASLESVRGNRS 72

Query: 321 LLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEKKKVLIRQNGTFFV 500
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Sbjct: 73 LFTDLEAENDVLHCVAFAVPK-SSSNEEVNFLTQVKGPTQEFKKRTTVMVKNEDSLVPV 131

Query: 501 QTDKPLYTPGQQVYFRIVTMDSNFVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLS 680
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S
Sbjct: 132 QTDKSIYKPGQTVKFRVVSMDENFHLPLVYIQDPKGNRIAQWQSFQLEGGGLKQFS 191

Query: 681 FQLAPEAMLGTYTVAE---GKTFGTFSVEEYVLPKFKVEWVEPKELSTVQESFLVKIC 851
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Sbjct: 192 FPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFEVQVTPVKIITILEEEMNVSV 251

Query: 852 CRYTYGKPMLGAVQVSVCKANTYWYREVEREQLPDKCNLSGQTDKTCGFSAPVDMATF 1031
 YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Sbjct: 252 GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCCKFSGQLNSHGCFYQQVTKVVF 309

Query: 1032 DLIGYAYSHQINIVATVVEGTGVEANATQNIYISPMGSMTEFDTSNFYHPNFPFSGKI 1211
 L Y +++ A + EGT VE Q+ I+ + ++F + + + PF G++
Sbjct: 310 QLKRKEYEMKHLTEAQIQEETVVELTGRQSSEITRTITKLSFKVKVDSHFRQGIPTFGQV 369

Query: 1212 RVRGHDDSFLLKNHLVFLVIYGTNGTFTNQTLVTDNNGLAPFTLETSGWNGTQDVSLGKPFQM 1391
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Sbjct: 370 RLVDGKGVPIPNKVIF--IRGNEANYSNATDEHGLVQFSINTTNVMGTSLTVRVNYKD 427

Query: 1392 EDLVYNPEQVPYRYQNAVYHLRPFYSTTFSFLGIHRLNGPLKCGQPQEVLDVYIDPADA 1571
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Sbjct: 428 RSPCYGYQWVSEHEEAHTAYLVFSPKSFVHLEPMSELPCGHTQTQVAHYILNGGTL 487

Fig. 4A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: 1572 SPDQEIFSYYLIGKSLVMEQGKHLNSKKGLKASFSLSLTFTSRSLAPDPSLVIYAI 1751
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKLSFYLLIMAKGIVRTGTHGLLVKQEDMKGHFSISIPVKSDIAPVARLLIYAVLP 547

Query: 1752 SGGVVADKIQFSVEMCFDNQVSLGFSQSPQQLPGAELQLQAAPGSLCALRAVD 1931
      +G V+ D ++ VE C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1932 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWDFPQPLIDPMPQGHSSQ 2111
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 2112 RP-SFSEGTDLFSFFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGAG 2252
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSTNEKDMYSFLEDMGLKAFNTSKIRPKMCPQLQQYEMHGPGLRVGFYESDV-MG 714

Query: 2253 GGHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEWKAMSF 2432
      GH P H VR+YF ETW+WDL + ++G V VTVPD ITEWKA +F
Sbjct: 715 RGHARLVHVEEP-HT---ETVRKYFAETWIWDLVVVNSAGVAEVGVTVPDITTEWKAGAF 770

Query: 2433 CTSQSRGFLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATIFNVLKDCIRV 2594
      C S+ G G+S T L AF+EFFV+LT+PYSV+RGE+F L AT+ NYL CIRV
Sbjct: 771 CLSEDAGLGISSTASLRAFQPFVVELTMPYSVIRGEAFTLKATVNLNLPKCIRV 824

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Fig. 4B